

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/189, 415C
Source: TFW 16
Date Processed by STIC: 08/05/2005

ENTERED



ZFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/189,415C

DATE: 08/05/2005

TIME: 16:37:08

Input Set : D:\UBCV0004.ST25.txt
 Output Set: N:\CRF4\08052005\I189415C.raw

3 <110> APPLICANT: Finlay, Brett B.
 4 Kenny, Brandt
 5 DeVinney, Rebekah
 6 Stein, Marcus
 8 <120> TITLE OF INVENTION: HOST RECEPTOR FOR PATHOGENIC BACTERIA
 10 <130> FILE REFERENCE: UBCV-0004
 12 <140> CURRENT APPLICATION NUMBER: US 09/189,415C
 13 <141> CURRENT FILING DATE: 1998-11-10
 15 <150> PRIOR APPLICATION NUMBER: US 60/065,130
 16 <151> PRIOR FILING DATE: 1997-11-12
 18 <160> NUMBER OF SEQ ID NOS: 14
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1920
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Escherichia coli
 27 <400> SEQUENCE: 1
 28 cggctgcata ccattacgtc atagtaatat aaaggaacgt gtcaaatttc taaataaaag 60
 30 gatatatgtt tgccttattgg taaccttggtt aataatgttt atggcaatca tttaattccc 120
 32 cctcgccgc cactacccctt acaaacagac ggcgcggcac ggggaggaaac tggtcatcta 180
 34 attagctcta caggagcatt agatctcgat tcatttttt ctccccctgag aaattctatg 240
 36 gctgattctg tcgattccag agatattcca ggacttccta caaacccatc gaggttgct 300
 38 gcaagctacat ctgagacatg cttgcttggg ggatttgaag ttctccatga taagggcca 360
 40 ctttatatttc tcaatacgca aattggacc tctgcatttc gtgttgaagt gcaggcagat 420
 42 ggtactcatg cgcattttgg agaaaaaaaat ggtttggagg ttagcgttac attaagtcc 480
 44 caagaatggc gcagcttgca atctattgtt actgagggtt aaaaacagatt tgttttacc 540
 46 gggggacgtg gcggttgttgg gcatccgtat gtcactgtcg catcagatat cgccggaaagct 600
 48 cgtacgaaaa tactggccaa attagacccaa gacaatcatg gaggacgtca acccaaggac 660
 50 gttgatacgc gttctgttgg tggccgcgc gtttcggaa tagatgttgg cgttgttagc 720
 52 gaaacccata cttcaacaac aaattccagc gttcgctcag atcctaaatt ctgggtttct 780
 54 gtcggcgccaa ttgttgttgg tttagcgggaa ctggccgaa ctgggtattgc acaggcgtt 840
 56 gcttgcacac cggaaaccggaa tgatcctaca accaccgtat ctgatcaggc cgccaaatgct 900
 58 gcagaaaatgtt caacaaaaaga tcagttaaacg caagaagcat tcaagaaccc tgagaaccag 960
 60 aaagttaaca tcgatgcgaa cgaaatgtt attccgtctg gggaaattaaa agatgttattt 1020
 62 gttgagcaaa tagcacaaca agctaaagag gctgggttggg tggccagaca gcaggctgtt 1080
 64 gaaagcaatg cacaggcgca gcagcgatat gaggatcagc atgccagacg tcaggaggaa 1140
 66 ttacagctt catcggtat tggttacggc ctcagcgtt cattgttgg tgcgtgggg 1200
 68 attgggtgtt ggttaacgcgat tgcgttccat agacgaaatc agccggcaga acagacaact 1260
 70 actacaacaa cacatacggtt agtgcagca cagaccggag ggataccccca gcacaagggtt 1320
 72 gcaactgtgc cacaagagcg aagacgttcc tctgtatagac gtgattcgca ggggagtgtt 1380
 74 gcatcgacac actgggtcaga ttccctctagc gaagtggta atccatatgc tgaagttggg 1440
 76 gggctcgga atagtctatc ggctcatcag ccagaagagc atatttatga tgaggctcgat 1500
 78 gcagatcctg gttatagcgttattcagaat tttcaggaa gcggcccgat taccggaaagg 1560

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80 ttaataggaa ctccagggca aggtatccaa agtacttatg cgcttctggc aaacagcggc 1620
 82 ggattgcgtt taggtatggg aggattaacg agtgggtggcg agacggcagt aagtctgt 1680
 84 aatgccgcac caacgcagg accagtacgt ttcggtttaaa tatatctgtg agtatttagt 1740
 86 tgagggtggg gtgggtggg gggcggttt actacgtta atgttcaga gaacaacgtt 1800
 88 gcagcatggg taactcttga acttctgtta ttataatcaa ttaagagaaa ttataatgtc 1860
 90 atcaagatat gaactttat tagataggtt tgcggaaaaa attggtgtt gatctatttc 1920
 93 <210> SEQ ID NO: 2
 94 <211> LENGTH: 549
 95 <212> TYPE: PRT
 96 <213> ORGANISM: Escherichia coli
 99 <220> FEATURE:
 100 <221> NAME/KEY: misc_feature
 101 <222> LOCATION: (314)..(314)
 102 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 104 <400> SEQUENCE: 2
 106 Met Pro Ile Gly Asn Leu Gly Asn Asn Val Asn Gly Asn His Leu Ile
 107 1 5 10 15
 110 Pro Pro Ala Pro Pro Leu Pro Ser Gln Thr Asp Gly Ala Ala Arg 'Gly
 111 20 25 30
 114 Gly Thr Gly His Leu Ile Ser Ser Thr Gly Ala Leu Gly Ser Arg Ser
 115 35 40 45
 118 Leu Phe Ser Pro Leu Arg Asn Ser Met Ala Asp Ser Val Asp Ser Arg
 119 50 55 60
 122 Asp Ile Pro Gly Leu Pro Thr Asn Pro Ser Arg Leu Ala Ala Ala Thr
 123 65 70 75 80
 126 Ser Glu Thr Cys Leu Leu Gly Gly Phe Glu Val Leu His Asp Lys Gly
 127 85 90 95
 130 Pro Leu Asp Ile Leu Asn Thr Gln Ile Gly Pro Ser Ala Phe Arg Val
 131 100 105 110
 134 Glu Val Gln Ala Asp Gly Thr His Ala Ala Ile Gly Glu Lys Asn Gly
 135 115 120 125
 138 Leu Glu Val Ser Val Thr Leu Ser Pro Gln Glu Trp Ser Ser Leu Gln
 139 130 135 140
 142 Ser Ile Asp Thr Glu Gly Lys Asn Arg Phe Val Phe Thr Gly Gly Arg
 143 145 150 155 160
 146 Gly Gly Ser Gly His Pro Met Val Thr Val Ala Ser Asp Ile Ala Glu
 147 165 170 175
 150 Ala Arg Thr Arg Ile Leu Ala Lys Leu Asp Pro Asp Asn His Gly Gly
 151 180 185 190
 154 Arg Gln Pro Lys Asp Val Asp Thr Arg Ser Val Gly Val Gly Ser Ala
 155 195 200 205
 158 Ser Gly Ile Asp Asp Gly Val Val Ser Glu Thr His Thr Ser Thr Thr
 159 210 215 220
 162 Asn Ser Ser Val Arg Ser Asp Pro Lys Phe Trp Val Ser Val Gly Ala
 163 225 230 235 240
 166 Ile Ala Ala Gly Leu Ala Gly Leu Ala Ala Thr Gly Ile Ala Gln Ala
 167 245 250 255
 170 Leu Ala Leu Thr Pro Glu Pro Asp Asp Pro Thr Thr Thr Asp Pro Asp
 171 260 265 270

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174 Gln Ala Ala Asn Ala Ala Glu Ser Ala Thr Lys Asp Gln Leu Thr Gln
 175 275 280 285
 178 Glu Ala Phe Lys Asn Pro Glu Asn Gln Lys Val Asn Ile Asp Ala Asn
 179 290 295 300
W--> 182 Gly Asn Ala Ile Pro Ser Gly Glu Leu Xaa Asp Asp Ile Val Glu Gln
 183 305 310 315 320
 186 Ile Ala Gln Gln Ala Lys Glu Ala Gly Glu Val Ala Arg Gln Gln Ala
 187 325 330 335
 190 Val Glu Ser Asn Ala Gln Ala Gln Gln Arg Tyr Glu Asp Gln His Ala
 191 340 345 350
 194 Arg Arg Gln Glu Glu Leu Gln Leu Ser Ser Gly Ile Gly Tyr Gly Leu
 195 355 360 365
 198 Ser Ser Ala Leu Ile Val Ala Gly Gly Ile Gly Ala Gly Val Thr Thr
 199 370 375 380
 202 Ala Leu His Arg Arg Asn Gln Pro Ala Glu Gln Thr Thr Thr Thr
 203 385 390 395 400
 206 Thr His Thr Val Val Gln Gln Gln Thr Gly Gly Ile Pro Gln His Lys
 207 405 410 415
 210 Val Ala Leu Met Pro Gln Glu Arg Arg Phe Ser Asp Arg Arg Asp
 211 420 425 430
 214 Ser Gln Gly Ser Val Ala Ser Thr His Trp Ser Asp Ser Ser Ser Glu
 215 435 440 445
 218 Val Val Asn Pro Tyr Ala Glu Val Gly Gly Ala Arg Asn Ser Leu Ser
 219 450 455 460
 222 Ala His Gln Pro Glu Glu His Ile Tyr Asp Glu Val Ala Ala Asp Pro
 223 465 470 475 480
 226 Gly Tyr Ser Val Ile Gln Asn Phe Ser Gly Ser Gly Pro Val Thr Gly
 227 485 490 495
 230 Arg Leu Ile Gly Thr Pro Gly Gln Gly Ile Gln Ser Thr Tyr Ala Leu
 231 500 505 510
 234 Leu Ala Asn Ser Gly Gly Leu Arg Leu Gly Met Gly Gly Leu Thr Ser
 235 515 520 525
 238 Gly Gly Glu Thr Ala Val Ser Ser Val Asn Ala Ala Pro Thr Pro Gly
 239 530 535 540
 242 Pro Val Arg Phe Val
 243 545
 246 <210> SEQ ID NO: 3
 247 <211> LENGTH: 1723
 248 <212> TYPE: DNA
 249 <213> ORGANISM: Escherichia coli
 251 <400> SEQUENCE: 3
 252 atgcctattg gtaaccttgg tcataatccc aatgtgaata attcaattcc tcctgcacct 60
 254 ccattacctt cacaaacccgca cggtgtcagg gggcggtggtc agctcattaa ctctacgggg 120
 256 ccgttggat ctcgtgcgtt atttacgcct gtaaggaatt ctatggctga ttctggcgac 180
 258 aatcgtgccca gtgatgttcc tggacttctt gtaaatccgca tgccgcctggc ggcgtctgag 240
 260 ataacactga atgatggatt tgaagttctt catgatcatg gtccgcctcgaa tactcttaac 300
 262 aggcagattt gctcttcgggtt atttcgagg gaaactcagg aagatggtaa acatatttgct 360
 264 gtcgggtcaga ggaatgggtgt tgagacctt gttgtttaa gtgatcaaga gtacgctcgc 420
 266 ttgcagtcca ttgatcctga aggtaaagac aaatttgat ttactggagg ccgtgggtgg 480

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268	gctgggcatg	ctatggtcac	cgttgcttca	gatatcacgg	aagcccccca	aaggatactg	540
270	gagctgttag	agcccaaagg	gaccggggag	tccaaaggtg	ctggggagtc	aaaaggcggtt	600
272	ggggagttga	gggagtcaaa	tagcggtgcg	gaaaacacca	cagaaactca	gacctcaacc	660
274	tcaacttcca	gccttcgttc	agatcctaaa	ctttgggtgg	cgttggggac	tgttgctaca	720
276	ggctctgatag	ggttggcggc	gacgggtatt	gtacaggcgc	ttgcattgac	gccggagccg	780
278	gatagcccaa	ccacgaccga	ccctgatgca	gctgcaagtg	caactgaaac	tgcgacaaga	840
280	gatcagttaa	cgaaaagaagc	gttccagaaac	ccagataatc	aaaaagttaa	tatcgatgag	900
282	ctcgaaatag	cgattccgtc	aggggttattg	aaagatgatg	tttgtgcgaa	tatagaagag	960
284	caggctaaag	cagcaggcga	agaggccaaa	cagcaagcca	ttgaaaataa	tgctcaggcg	1020
286	aaaaaaaaat	atgatgaaca	acaagctaaa	cgccaggagg	agctgaaagt	ttcatcgggg	1080
288	gctggctacg	gtcttagtgg	cgcattgatt	cttgggtggg	gaattgggt	tgcgtcacc	1140
290	gctgcgttc	atcgaaaaaa	ttagccggta	gaacaaacaa	caacaactac	tactacaact	1200
292	acaactacaa	gcmcacgtac	gtagagaaat	aagcctgca	ataatacacc	tgcacagggc	1260
294	aatgttagata	cccctgggtc	agaagatacc	atggagagca	gacgtagctc	gatggctagc	1320
296	acctcgtcga	ctttcttga	cacttccagc	atagggaccg	tgcagaatcc	gtatgctgat	1380
298	gttaaaacat	cgctgcatga	ttagccgggt	ccgacttcta	attctaatac	gtctgttcag	1440
300	aatatgggaa	atacagattc	tgttgtatat	agcaccattc	aacatcctcc	ccgggatact	1500
302	actgataacg	gcmcacgggtt	attagggaaat	ccaagtgcgg	ggattcaag	cacttatgcg	1560
304	cgtctggcgc	taagtgggtt	attacgcccatt	gacatgggg	gattaacggg	ggggagtaat	1620
306	agcgctgtga	atacttcgaa	taacccacca	gcmcacggat	cccatcggtt	cgtctaaata	1680
308	tatccataat	cattttat	agagggaggg	aggggggaag	tct		1723

311 <210> SEQ ID NO: 4

312 <211> LENGTH: 559

313 <212> TYPE: PRT

314 <213> ORGANISM: Escherichia coli

316 <400> SEQUENCE: 4

318	Met Pro Ile Gly Asn Leu Gly His Asn Pro Asn Val Asn Asn Ser Ile						
319	1	5	10	15			
322	Pro Pro Ala Pro Pro Leu Pro Ser Gln Thr Asp Gly Ala Gly Gly Arg						
323	20	25	30				
326	Gly Gln Leu Ile Asn Ser Thr Gly Pro Leu Gly Ser Arg Ala Leu Phe						
327	35	40	45				
330	Thr Pro Val Arg Asn Ser Met Ala Asp Ser Gly Asp Asn Arg Ala Ser						
331	50	55	60				
334	Asp Val Pro Gly Leu Pro Val Asn Pro Met Arg Leu Ala Ala Ser Glu						
335	65	70	75	80			
338	Ile Thr Leu Asn Asp Gly Phe Glu Val Leu His Asp His Gly Pro Leu						
339	85	90	95				
342	Asp Thr Leu Asn Arg Gln Ile Gly Ser Ser Val Phe Arg Val Glu Thr						
343	100	105	110				
346	Gln Glu Asp Gly Lys His Ile Ala Val Gly Gln Arg Asn Gly Val Glu						
347	115	120	125				
350	Thr Ser Val Val Leu Ser Asp Gln Glu Tyr Ala Arg Leu Gln Ser Ile						
351	130	135	140				
354	Asp Pro Glu Gly Lys Asp Lys Phe Val Phe Thr Gly Gly Arg Gly Gly						
355	145	150	155	160			
358	Ala Gly His Ala Met Val Thr Val Ala Ser Asp Ile Thr Glu Ala Arg						
359	165	170	175				
362	Gln Arg Ile Leu Glu Leu Glu Pro Lys Gly Thr Gly Glu Ser Lys						

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363	180	185	190
366	Gly Ala Gly Glu Ser Lys Gly Val	Gly Glu Leu Arg	Glu Ser Asn Ser
367	195	200	205
370	Gly Ala Glu Asn Thr Thr	Glu Thr Gln Thr	Ser Thr Ser Thr Ser Ser
371	210	215	220
374	Leu Arg Ser Asp Pro Lys	Leu Trp Leu Ala	Leu Gly Thr Val Ala Thr
375	225	230	235
378	Gly Leu Ile Gly Leu Ala Ala	Thr Gly Ile Val	Gln Ala Leu Ala Leu
379	245	250	255
382	Thr Pro Glu Pro Asp Ser Pro	Thr Thr Asp Pro Asp	Ala Ala Ala
383	260	265	270
386	Ser Ala Thr Glu Thr Ala Thr	Arg Asp Gln Leu	Thr Lys Glu Ala Phe
387	275	280	285
390	Gln Asn Pro Asp Asn Gln	Lys Val Asn Ile Asp	Glu Leu Gly Asn Ala
391	290	295	300
394	Ile Pro Ser Gly Val Leu	Lys Asp Asp Val	Val Ala Asn Ile Glu Glu
395	305	310	315
398	Gln Ala Lys Ala Ala Gly	Glu Glu Ala Lys	Gln Gln Ala Ile Glu Asn
399	325	330	335
402	Asn Ala Gln Ala Gln Lys	Lys Tyr Asp Glu Gln	Gln Ala Lys Arg Gln
403	340	345	350
406	Glu Glu Leu Lys Val Ser	Ser Gly Ala Gly	Tyr Gly Leu Ser Gly Ala
407	355	360	365
410	Leu Ile Leu Gly Gly	Ile Gly Val Ala Val	Thr Ala Ala Leu His
411	370	375	380
414	Arg Lys Asn Gln Pro Val	Glu Gln Thr Thr	Thr Thr Thr Thr Thr Thr
415	385	390	395
418	405	410	415
422	Thr Thr Thr Ser Ala Arg	Thr Val Glu Asn	Lys Pro Ala Asn Asn Thr
423	420	425	430
426	Ser Arg Arg Ser Ser Met	Ala Ser Thr Ser	Ser Thr Phe Phe Asp Thr
427	435	440	445
430	Ser Ser Ile Gly Gly	Pro Cys Arg Ile Arg	Met Leu Met Leu Lys His
431	450	455	460
434	Arg Cys Met Ile Arg Arg	Cys Arg Leu Leu	Ile Leu Ile Arg Leu Phe
435	465	470	475
438	485	490	495
442	Arg Ile Trp Gly Ile	Gln Ile Ser Val Val	Tyr Ser Thr Ile Gln His
443	500	505	510
446	Leu Arg His Asp Met	Gly Gly Leu Thr	Gly Gly Ser Asn Ser Ala Val
447	515	520	525
450	530	535	540
454	Asn Thr Ser Asn Asn	Pro Pro Ala Pro	Gly Ser His Arg Phe Val
455	545	550	555
458	<210> SEQ ID NO: 5		
459	<211> LENGTH: 1460		

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/05/2005
PATENT APPLICATION: US/09/189,415C TIME: 16:37:09

Input Set : D:\UBCV0004.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 314

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9

VERIFICATION SUMMARY

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L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:304